

STIC-Biot ch/ChemLib

83130

From: Li, Ruixiang
Sent: Friday, December 27, 2002 2:28 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application NO: 09/898,586

Please do a standard search on SEQ ID NO: 24 against interference nucleic acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
CM1 10E18
Mail Box 10D19
306-0282

Point of Contact:
Toby Fort
Technical Info. Specialist
CM1 6A04
703-308-3534

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 1/2
Date Completed: 1/9
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____



ALIGNMENTS

```

RESULT 1
: Sequence 41,
: GENERAL INFORMATION:
: APPLICANT: INCYTE GENOMICS, INC.
: APPLICANT: KU-YOUNG, Janice
: APPLICANT: BANDMAN, Olga
: APPLICANT: TANG, Y. Tom
: APPLICANT: YUE, Henry
: APPLICANT: AZIMZAI, Yalda
: APPLICANT: BUREFORD, Neil
: APPLICANT: BAUGHN, Mariah R.
: APPLICANT: LU, Dzung Aina M.
: APPLICANT: HITLMAN, Jennifer L.
: APPLICANT: PATTERSON, Chandra
: APPLICANT: LAL, Preethi
: TITLE OF INVENTION: RECEPTORS AND ASSOCIATED PROTEINS
: FILE REFERENCE: PF-0726 PCT
:
: PRIOR APPLICATION NUMBER: 60/145,232; 60/158,578; 60/165,192
: PRIOR FILING DATE: 1999-07-21; 1999-10-07; 1999-11-12
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: PERL Program
: SEQ ID NO 41
: LENGTH: 974
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature

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US-09-898-586-24 (1-310) x 1
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Score: 1609.00 Matches: 310
Percent Similarity: 100.008 Conservative: 0
Best Local Similarity: 100.008 Mismatches: 0
Query Match: 100.008 Indels: 0
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Qy 21 ArgIleGlnMetLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuGly 40
Db 61 AGGATTCAGATGCTCTCTTTGGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Qy 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhe 60
Db 121 AACGGGACCAATAGTGGGCTCATCTCACTGACTCCAGACTCCAGCCCATGATCTTC 180
Qy 61 PheLeuSerHisLeuAlaValAlaValAspIleAlaTyrAlaCysAsnThrValProArgMet 80
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Qy 81 LeuValAsnLeuLeuHisProAlaValProIleSerPheAlaGlyArgMetMetGlyThr 100
Db 241 CTGGTGAACCTCTGCTCATCCAGCCAGCCCATCTCTTGGGGGCGGCGCATGACAGACC 300
Qy 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAsp 120
Db 301 TTCTCTTTCACATTTTGGCTGTCACAGAAATGCTCTCTCTCTCTCTCTCTCTCTCT 360
Qy 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTyrPyrAlaCys 140
Db 361 CTGACGTGGCCATCTGCCACCCCTCCGATTTGGCCATCATGAGAACATGGCTCTTGGCC 420
Qy 141 IleThrLeuAlaValThrSerTyrThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 421 ATCACCCCTGGCGGTGACTTCCTGGACACATGAGTCTTTTATCTGATATGATCTTGTG 480
Qy 161 LeuLeuLeuProLeuProPheCysArgProGlnArgIleTyrHisPhePheCysIle 180
Db 481 TTACTTCACCTTACCTTCTGTTGGCCCAAGAAATTTATCATCTTTTGTGTAATTC 540
Qy 181 LeuAlaValLeuLeuLeuAlaCysAlaAspThrHisIleAsnGlnAsnMetValLeuAla 200
Db 541 TTGGCTGTTCTCAACTTGCCTGTGCAGATACCCACATCATGAGAACATGGCTCTTGGCC 600
Qy 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValAlaSerTyrMetCysIle 220
Db 601 GGACCAATTTCTGGGCTGGTGGACCTTGTCCCAATTTGATTTTCATATATGAGCATC 660
Qy 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgGlyAlaPheCysThrCys 240
Db 661 CTGTGTCATCTCTGATCCATCCATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 700
Qy 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
Db 721 TTTCCTCCACCTCTGTGTGATTTGACTCTTTATGCGACACCATTTATCATGATATCTGGA 780
Qy 261 ProArgTyrGlyAsnProCysGlnGlnIleCysTyrLeuLeuLeuPheHisSerLeuPhe 280
Db 781 CCAGATATGGAGACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Qy 281 AspProMetLeuAspProLeuIleCysSerLeuArgAsnSerValAlaCysAsnThrLeu 300
Db 841 AATCCATGCTCATCTCTTATCTGTAGTCTTAGAGACTCAGAGAGAGAGAGAGAGAGAG 900
Qy 301 LysArgValLeuGlyValGlnArgAlaLeu 310
Db 901 AAGACAGCTCTGAGATATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960

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Fri Jan 3 14:36:52 2003

us-09-898-586-24.p2n.rn1

Page 1

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 2, 2003, 08:42:37 ; Search time 77 Seconds

(without alignments)
1234.673 Million cell updates/sec

Title: US-09-898-586-24

Perfect score: 1609
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-O=/cgn2_1/USPTO.spool/US09898586/runat.02012003.084227.19599/app.query.fasta.1.455
-DB=Issued_Patents.NA -QPMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=humand0.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODF=LOCAL -OUTFMT=pct -NORM=ext -HEARSTIE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09898586.ecgn_1.1.31.etrunc.02012003.084227.19599 -NCPD=6 -ICPD=3
-NO_XLPHY -NO_MAMP -LARGEORDER -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

Database :

1: Issued_Patents.NA:*
2: /cgn2_6/pdata/1/ina/5A.COMB.seq:*
3: /cgn2_6/pdata/1/ina/5B.COMB.seq:*
4: /cgn2_6/pdata/1/ina/6A.COMB.seq:*
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6: /cgn2_6/pdata/1/ina/PCITUS.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048.5	65.2	1713	2	US-08-467-948A-1
2	1048.5	65.2	1713	3	US-08-467-947A-1
3	609	37.8	966	3	US-08-748-506-5
4	606	37.7	1290	2	US-08-827-281A-1
5	605	37.6	1062	4	US-09-668-680-10
6	592	36.8	966	3	US-08-748-506-7
7	578	35.9	966	3	US-08-748-506-8
8	574	35.7	966	3	US-08-748-506-6
9	543	33.7	900	4	US-09-085-371-5
10	524	32.6	1297	4	US-09-668-680-11
11	521	32.4	1080	4	US-09-668-680-9
12	452	28.1	984	3	US-08-748-506-9

13	418.5	26.0	1539	4	US-09-668-680-13	Sequence 13, Appl
14	384	23.9	963	4	US-09-605-785-526	Sequence 526, App
15	384	23.9	963	4	US-09-439-313-526	Sequence 526, App
16	382.5	23.8	1828	3	US-08-988-876-2	Sequence 2, Appl
17	369	22.9	1474	1	US-08-465-960-1	Sequence 1, Appl
18	369	22.9	1474	2	US-09-053-303-1	Sequence 1, Appl
19	369	22.9	1474	4	US-09-339-115-1	Sequence 1, Appl
20	369	22.9	1474	5	PCT-US95-07093-1	Sequence 1, Appl
21	236	14.7	897	4	US-09-668-680-5	Sequence 5, Appl
22	185.5	11.5	978	3	US-08-706-281A-17	Sequence 17, Appl
23	185.5	11.5	978	4	US-08-671-525B-9	Sequence 17, Appl
24	182.5	11.3	975	1	US-08-672-109B-9	Sequence 9, Appl
25	182.5	11.3	975	1	US-08-672-109B-9	Sequence 9, Appl
26	182.5	11.3	975	1	US-08-842-045-9	Sequence 9, Appl
27	182.5	11.3	975	2	US-08-842-045-9	Sequence 9, Appl
28	182.5	11.3	975	3	US-08-629-335B-9	Sequence 9, Appl
29	181	11.2	1320	1	US-08-599-252-84	Sequence 84, Appl
30	181	11.2	1320	1	US-08-436-074-57	Sequence 57, Appl
31	181	11.2	1320	5	PCT-US96-06352-84	Sequence 84, Appl
32	181	11.2	1320	5	PCT-US96-06583-84	Sequence 84, Appl
33	179.5	11.2	1650	4	US-08-387-805-15	Sequence 15, Appl
34	175	10.9	999	4	US-08-870-511-7	Sequence 15, Appl
35	174.5	10.8	1080	1	US-08-671-525B-5	Sequence 5, Appl
36	174.5	10.8	1080	1	US-08-672-109B-5	Sequence 5, Appl
37	174.5	10.8	1080	1	US-08-842-045-5	Sequence 5, Appl
38	174.5	10.8	1080	1	US-08-842-045-5	Sequence 5, Appl
39	174.5	10.8	1080	2	US-08-842-238-5	Sequence 5, Appl
40	173	10.8	996	1	US-08-629-335B-5	Sequence 5, Appl
41	173	10.8	996	1	US-08-671-525B-7	Sequence 7, Appl
42	173	10.8	996	1	US-08-672-109B-7	Sequence 7, Appl
43	173	10.8	996	1	US-08-842-045-7	Sequence 7, Appl
44	173	10.8	996	2	US-08-842-238-7	Sequence 7, Appl
45	173	10.8	999	4	US-08-629-335B-7	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-08-467-948A-1
Sequence 1, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1713 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 116..1003
 US-08-467-948A-1

Alignment Scores:

Pred. No.: 1,29e-111 Length: 1713
 Score: 1048.50 Matches: 211
 Percent Similarity: 81.64% Conservative: 38
 Local Similarity: 69.18% Mismatches: 52
 Query Match: 65.16% Indels: 4
 Gaps: 1

US-09-898-586-24 (1-310) x US-08-467-948A-1 (1-1713)

QY 1 MetGlyAspAsnLleThrsSerLleThrsGluPheLeuLeuGlyPheProValGlyPro 20
 128 ATGTGTAATAATGACAGATGTCACAGATTCCTCTACTGGGATTCCTCCGGGCCCA 187
 QY 21 ArgLleGluMetLeuLeuPheGlyLeuPheSerLeuPheThyValPheThrLeuGly 40
 188 AGGATTCACATGCTCTCTTGGGCTTCCTGCTTCCTGATGCTTCACCTGCTGCGG 247
 QY 41 AsnGlyThrLleLeuGlyLeuLleSerLeuAspSerArgLeuHisAlaProMetThyPhe 60
 248 AATGGGACCATCTGGGGCTCATCTCAGCTCCAGACTCCAGACCCCATGATCTTC 307
 QY 61 PheLeuSerHisLeuAlaValAlaAspLleAlaThyAlaCysAsnThyValProArgMet 80
 308 TTCTCTCCACACCTGGCCCTGCTCAACATCCCTATGCTGCAACAGAGCCCGCAGATG 367
 QY 81 LeuValAsnLeuLeuHisProAlaLysProLleSerPheAlaGlyArgMetGluThr 100
 368 CTGGTGAACCTCCTGCATCCAGCCAGCCATCTCTTGGCTGTCATGACACTAGAC 427
 QY 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValAlaMetSerThyAsp 120
 428 TTCTCTTTTGGATTGTCACATACGTAATGCTCCGTTGGTGGTGCATGCTACGAT 487
 QY 121 LeuThyValAlaLleCysHisProLeuArgThyLeuAlaLleMetThrTrpArgValCys 140
 488 CGGTGAGTGGCCTGTCACCTCCGATATTCATCATCAGTACGACCTGGAAGCTGC 547
 QY 141 IleThrLeuAlaValThrSerTrpThrGlyValLeuLeuSerLeuLleHisLeuVal 160
 548 ATCACTCTGGGACATCTTCCCGGACATGTCCTCTGCGGTATGTCATCTGAGAC 607
 QY 161 LeuLeuLeuProLeuProPheCysArgProGluLysIleThyHisPhePheCysGluLe 180
 608 CTCATCTTAAGACTGCCCTTTGTGGGCTCTGTGAATCAACCACTCTCTGTGAATC 667
 QY 181 LeuAlaValLeuLeuAlaCysAlaAspThrHisLleAsnGluAsnMetValLleAla 200
 668 CTGTCTGCTCAAGCTGAGCTGCTGATACCTGGCTCAACAGGGTGCATCTTTGAA 727
 QY 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrLleValValSerThyMetCysIle 220
 728 GCCTGCATGTTCATCTGCTGGAGCACCTGCTGCTGGTGTCTCTCTACACATC 787
 QY 221 LeuCysAlaIleLeuGluLleGluLleSerArgGluValGlnArgGlyAlaPheCysThrCys 240

Db 788 CCGGGGGGACATCCATGACATCTGCGGAGGGCCGACGAAGGCCCTTCTCCACTCC 847
 QY 241 PheSerHisLeuCysValIleGlyLeuPheThyGlyThrAlaIleLleMetThyValGly 260
 Db 848 TCCTCCACCTCTGGGAGTGGGACTCTTCTTGGGAGCCCACTCTCATGACATGAGCC 907
 QY 261 ProArgThyGlyAsnProLysGluLysLysThyLeuLeuLeuPheHisSerLeuPhe 280
 Db 908 CCAAGTCCCGGCATCTCGAGAGCAGACAGAGAGTCTTCTTCTTATTTATACATTCCT 967
 QY 280 eAsnPro--MetLeuAsnProLeuLle-CysSerLeuArgAsnSerGlu-ValLysAsn 298
 Db 968 TCAACCCGATCTTAAACCCCTGATTTTACAACTGAGGAAATGTAAGGCTCAAGCT 1027
 QY 299 ThrLeuLys 301
 Db 1028 GCCCTCCGA 1036

RESULT 2

US-08-467-947A-1
 Sequence 1, Application US/08467947A
 Patent No. 6090575

GENERAL INFORMATION:

APPLICANT: LI, YI
 APPLICANT: CHU, LIANG
 APPLICANT: NI, JIAN
 APPLICANT: GENTZ, REINER
 APPLICANT: BOLT, CAROL J.
 APPLICANT: SUTTON III, GRANGER G.
 APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-protein
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,947A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04079

FILING DATE: 30-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: STERNE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1713 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 116..1003

US-08-467-947A-1

Alignment Scores:

Pred. No.: 1,29e-111 Length: 1713


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QY 123 VALAIAIIECYSHISProleuArgTyrLeuAlaIleMetThrTPRArgValCysIleThr 142
Db 388 ATGGCCATATGTCCTCCCATCTACACTATGCAACCCGAAAGGCTGGAGATTTGGCCCAT 447
QY 143 LeuAlaValThrSerTrpThrGlyValLeuLeuSerLeuIleHisLeuValLeuLeu 162
Db 448 TTGGCCATTTGTTTCATGGGGAATGGAGATAGTAAGCTGAGCAACAACCAATTTTAT 507
QY 163 LeuProLeuProPhoCysArgProGlnIleTyrHisIlePhePheCysGlnIleLeuAla 182
Db 508 TTCTCCTTGACCTTGATGAGCCCTGTGAATAATGACACTTCTTGACCTTCCACCT 567
QY 183 VALLeuLysLeuAlaCysAlaAspThrHisIleAsnGlnAsnMetValLeuAlaGlyAla 202
Db 568 CTCCTGGCACTTGCTCTGGAGATACATCCCAAAAGAGGCTGCCATCTTTGGTGCA 627
QY 203 IIEserGlyLeuValGlyProLeuSerThrIleValIleValSerTyrMetCysIleLeuCys 222
Db 628 GTCCCTGCATATCTAGCCCATTTTGGCTGATCATTTATCTTATGTCAAAATTTCTCAT 687
QY 223 AlaIleLeuGlnIleGlnSerArgGlnValGlnArgIleValIlePheCysThrCysPheSer 242
Db 688 GCAGTGCTCTGCTATGCTCTACCTGAGGCGGCATTAAGCTTTTGCACCTGTTCCTCT 747
QY 243 HisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGlyProArg 262
Db 748 CACCTACTGTATGTCACACTTTTATATGCTGACATGTATACCTATTTGAGGCCCAAG 807
QY 263 TyrGlyAsnProLysGlnGlnIleLysTyrIleLeuLeuPheHisSerLeuPheAsnPro 282
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QY 283 MetLeuAsnProLeuIleCysSerLeuArgAsnSerGlnValIleAsnThrLeuLysArg 302
Db 868 ATGCTACACCTCATCATATATGTTTAAAGAAACAAGAAAGCAAGCAGCAGCTGAGAGA 927
QY 303 VALLeuGlyValGlnArgAlaLeu 310
Db 928 ACTCTGGCGCTGAAAAAATTTCTG 951

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REFERENCE/DOCKET NUMBER: GP50001
TELEPHONE: 610-270-5015
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1290 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-827-291A-1

Alignment Scores:
Pred. No.: 1 33e-60 Length: 1290
Score: 606.00 Matches: 122
Percent Similarity: 59.87% Conservative: 60
Best Local Similarity: 40.13% Mismatches: 120
Query Match: 37.66% Indels: 2
DB: 2 Gaps: 2

US-09-898-586-24 (1-310) x US-08-827-291A-1 (1-1290)
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QY 22 IIEGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValIleThrIleLeuGlyAsn 41
Db 365 CACACCTTCTCTTCTGCTGCTGCGCATCTTTCATG---GCCCTTACGGGAAC 421
QY 42 GltThrIleLeuGlyLeuIIEserLeuAspSerArgLeuHisAlaProMetTyrPhePhe 61
Db 422 TCTGTACAGTCTCTCTATCTACCTGACACCCAGCTCCACCCCATGACTCTCTC 481
QY 62 LeuSerHisIleLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMetLeu 81
Db 482 CTCAGCAACATGCTCCCTCATGACCTCATGCTCATCTGACACCCATACCAAGATGCC 541
QY 82 VALAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetGlnIlePhe 101
Db 542 TTCACACTACTGCTGCGGACAGATCCATTTCTATGCTGTGGTCACACAAATTTTC 601
QY 102 LeuPheSerThrPheAlaValThrGlnCysLeuLeuValValMetSerTyrAspLeu 121
Db 602 TTCTATACATGACTGCTGGCTGGAATGCTTCTTTGGCTGTATGCTGTATGACCGC 661
QY 122 TyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTPRArgValCysIle 141
Db 662 TACACTGCCATTTGCCACCCCTGAAGATACACCAATCTCATGACGCCCTAAATTTGTGA 721
QY 142 ThrLeuAlaValThrSerTrpThrGlyValLeuLeuSerLeuIleHisLeuValLeu 161
Db 722 CTTAGACTGCGCTTTCTCGATCGCTCGCTACAGATGAAATCATTTATGCTAGACC 781
QY 162 LeuLeuProLeuProPhoCysArgProGlnIleTyrHisIlePhePheCysGlnIleLeu 181
Db 782 ACATTTCTCTCTCTCTACGTGCGTCTGGAAATAGCCCTTCTGTGTGGATTACT 841
QY 182 AlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGlnAsnMetValLeuAlaGly 201
Db 842 TCCCTACTAAATCTCTCTGCAATGACACATCATATTTGAAAGGTTATTTTCATTTGC 901
QY 202 AlaIIEserGlyLeuValGlyProLeuSerThrIleValIleValSerTyrMetCysIleLeu 221
Db 902 TCTATAGTAATGCTTCTCTCCCTGTCATCATCATGCTTCTTATGCTGGAGTAT 961
QY 222 CysAlaIleLeuGlnIleGlnSerArgGlnValGlnArgIleValIlePheCysThrCysPhe 241
Db 962 CTGCGTGTATTCACATGAGCATCTGGAAGGCTGCGCAAGCTTTCACAGACCTGTCC 1021
QY 242 SerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGlyPro 261

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DB 1022 TCTCACCCTGATGGTGGATGTTCTATGACGAGCTTGCTATACATACAGCC 1081
QY 262 ARGTYGGLYAsnProlysgluInlyslstyIleuLeuPheHisSerLeuPheAsn 281
DB 1082 ACATGTGATGCTCCCAACGAGCAAGAGCTGGTGTCTGTATCTACCATCTGACT 1141
QY 282 PrometleuAsnProleuIleCysSerLeuArgAsnSerGluValIysAsnThrLeuIys 301
DB 1142 CCCATGCTGAATCCCTCATCTACAGCCTCCGCAACAGAGATGACCAAGATTCATG 1201
QY 302 ArgValLeuGly 305
DB 1202 AAGATCTCAGGA 1213

RESULT 5
US-09-668-680-10
; Sequence 10, Application US/09668680
Patent No. 6436703
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Wang, Jian-Rui
APPLICANT: Xue, Aidong J.
APPLICANT: Xu, Chongjun
APPLICANT: Dimaenac, Radoje T.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790CIP2A
CURRENT APPLICATION NUMBER: US/09/668, 680
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PL_FL_genes Version 2.0
SEQ ID NO 10
LENGTH: 1062
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1062)
-09-668-680-10

Alignment Scores:
Pred. No.: 1,296-60 Length: 1062
Score: 605.00 Matches: 126
Percent Similarity: 61.06% Conservative: 59
Best Local Similarity: 41.58% Mismatches: 114
Query Match: 37.60% Indels: 4
DB: 4 Gaps: 2

US-09-898-586-24 (1-310) x US-09-668-680-10 (1-1062)
QY 4 AsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyProArgIleGln 23
DB 136 AACCAACAGAGATTCTTGAAGTTTACCTTCGAGCTCTGAGAGATCCAGACTACAG 195
QY 24 MetLeuLeuPheGlyLeuPheSerLeuPheTyValPheThrLeuLeuGlyAsnGlyThr 43
DB 196 CCGTTTATTTGGGCTGTCTCTGTCATGTACCTGGGAGCGTCTGGAAACCTGCTC 255
QY 44 IleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaPrometLeuTyPhePheLeuSer 63
DB 256 ATCATCTGGCATCAGCTGATCCCACTCCACACCCCATGACTTCTCTCTCTCC 315
QY 64 HisLeuAlaValAlaSerIleAlaTyValAcGAsnThrValProArgMetLeuValAsn 83
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DB 316 AACCTGCTCCGAGTTCATCTGTTTCAGCACTTGCTCATGTCCTCCCAAGATGCTGTGAC 375
QY 84 LeuLeuHisProAlaIysProIleSerPheAlaGlyArgMetMetGlnThrPheLeuPhe 103
DB 376 ATCCAGACCCAGAACAAACCCATCTCTACATGAGCTGCCCTCCACAGAGCTATTTCTCC 435
QY 104 SerThrPheAlaValThrGluCysLeuLeuValValMetSerTyPhePheTyVal 123
DB 436 ARGTTTTCTATTCCTGACACCGCTACTGACCGGATGAGCGGCTTATGACCGGTTGTG 495
QY 124 AlaIleCysHisProLeuArgTyIleuAlaIleMetThrPheArgValCysIleThrLeu 143
DB 496 GCTGTCTGCCACCTCTGACATATGATCATCAAGAAACCCCACTCTGTGGCTCTG 555
QY 144 AlaValThrSerThrThrThrGlyValIleLeuSerLeuIleHisIleValIleLeu 163
DB 556 GTTTTGTACCTGCGGTATGTTGTGTACATGACATCCCTCCATATTTCTCATGTATG 615
QY 164 ProLeuProPheCysArgProGluInlyslIeTyHisPhePheCysGluIleLeuAlaVal 183
DB 616 CATCTATCTCTGTAAAGATTGTAATCCACATTTTCTGTGGAAGTACGCTACATC 675
QY 184 LeuIysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValIleAlaIle 203
DB 676 CTCACACTGCGCTGCTGATACCTTCCTGAAACACAGGTGATTTAC-----TTTATG 729
QY 204 SerGlyLeuValGly-----ProLeuSerThrIleValIleValSerTyMetCysIleLeu 721
DB 730 ACGGTGCTGCTGGCGTTTTCCTCTGGAACATTTCTTATTCAGGAATTCCT 789
QY 222 CysAlaIleLeuGlnIleGlnSerArgIleValGlnArgIleValAlaPheCysThrCysPhe 241
DB 790 TCATTCATAGAAGAAATGCTCATCTGCGGGAACAAACAAAGCACTTCCACCTGTGG 849
QY 242 SerHisLeuCysValIleGlyLeuPheTyGlyThrAlaIleIleMetTyValGlyPro 261
DB 850 TCTCACCCTCGCTGCTTCTTATTTATGGACAGCATGGGGTCCACTTCTCT 909
QY 262 ArgTyGlyAsnProlysgluInlyslstyIleuLeuLeuPheHisSerLeuPheAsn 281
DB 910 GCGGTACCTACCTTCCAGAAATCTCCGCTCGGTGATGATACATGCTGTGACCC 969
QY 282 PrometleuAsnProleuIleCysSerLeuArgAsnSerGluValIysAsnThrLeuIys 301
DB 970 CCCATCTTGAACCCCTTCTACAGCCTGAGAGACAGAGATGTGAAGAGAGCCCTGGG 1029
QY 302 ArgValLeu 304
DB 1030 AGTCTCTC 1038

RESULT 6
US-08-748-506-7
; Sequence 7, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
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Db	28	GAGAAATAGTTGTGTCAAAACGTTTGGCATTTGGCCAAAGTCTGTGAGGTCCCTGGAGAA	87
Qy	23	GLMetLeuLeuPhcGlyLeuPhSerLeuPhThyValPhcThLeuLeuGlyAsnGly	42
Db	88	TGCTTCTCTCTCTGACCCCTCATCTTCTCTCATGTTCTGTGATCTCAACGAAATGCT	147
Qy	43	Thh1LeuGlyLeu1LeSerLeuAspSerArgLeuHisAlaProMetLeuPhcLeu	62
Db	148	CTCATAGACCCCTGGATTTTGTACCAAGTCATCTCTACACACCCCACTGATCTTTCTG	207
Qy	63	SerHisLeuAlaValAspIleAlaIleThyAlaCysAsnThValProArgMetLeuVal	82
Db	208	GCCCACTTCTCTCTCTGGAATTTGGGTAATCTTGGCTGTATCTCATCCCAATGCTCTCAG	267
Qy	83	AspLeuLeuHisProAlaIleProIleSerPhaAlaGlyArgMetMetGlyThPhcLeu	102
Db	268	AGCTCTGTGAGAGGAGCCCGAGAGATCTTTCCAGTGGGATGGCCACACAGATGTTTTC	327
Db	103	PhaSerThrPhaAlaValThrGlyCysLeuLeuLeuValValMetSerThyAspLeuTyr	122
Db	328	TTCATATTTCTTTGGATTAAGTAGAGTGGCTCTTGGCAGCCATGAGCCTTGGACCGTAT	387
Qy	123	ValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrPArgValCysIleThr	142
Db	388	ATGGCATATGTTTCCCACTGCACTAGTACCAACCCGAATGAGTCGTAGATATGGCCAC	447
Qy	143	LeuAlaValAlaThrSerTrpThrGlyValLeuLeuSerLeuIleHisLeuValLeuLeu	162
Db	448	TTGGCAATTTCTTCTCATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT	507
Qy	163	LeuProLeuProPhcArgCysArgProGlyLeuIleThyHisPhcPhcCysGlyIleLeuAla	182
Db	508	TTCCTCTGCACTCTGTGAGACCCGTGAGATAGACCACTCTCTGTGATCTTCCACT	567
Qy	183	ValLeuLeuLeuAlaCysAlaAspThrHisIleAsnGlyAsnMetValLeuAlaGlyAla	202
Db	568	CTCTCTGCACTGCTGCTGTGATACATCCCAATTTGAGGCTGCCATCTTTGGTAGTT	627
Qy	203	IleSerGlyLeuValGlyProLeuSerThrIleValAlaValSerTyrMetCysIleLeuCys	222
Db	628	GTCTCTGCACTATCTAGACCCCTTTTGTCTGATCATTTATCTTATGTACGAATCTCTGTT	687
Qy	223	AlaIleLeuGlnIleGlnSerArgGlyValAlaGlnArgValAlaPhcCysThCysPhSer	242
Db	688	GCAAGTCCTGTGATGACCTTCACTGAGGGGCGCCACAAACCCCTTTCACCTGTCTCCCT	747
Qy	243	HisLeuCysValIleGlyLeuPhThyGlyThrAlaIleIleMetTyrValGlyProArg	262
Db	748	CACCTATCTGTAGTGCACACTCTTTTATGGGTCAGAGATCTGTATCACTATTGGAGGCTAG	807
Qy	263	TyrGlyAsnProLysGlnGlnLysTyrLeuLeuLeuPhcHisSerLeuPhcAsnPro	282
Db	808	TCTAGCCACTACCAAGGATGACAACTGTGGCTCTTCTACACAGCATGACATCC	867
Qy	283	MetLeuAsnProLeuIleCysSerLeuArgAsnSerGlyValAlaLysAsnThrLeuLysArg	302
Db	868	ATGTTGACCACTATCATCTATAGTTTAAAGAACAGAGATCTCAGGACGACACTGAAAGA	927
Qy	303	ValLeuGlyValGlnArgAlaLeu	310
Db	928	ATTCTGGCCCTGAAAAAATTTCTG	951

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1 STREET: Two Prudential Plaza, Suite 4900
2 CITY: Chicago
3 STATE: IL
4 COUNTRY: US
5 ZIP: 60601-6780
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Floppy disk
8 COMPUTER: IBM PC compatible
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10 SOFTWARE: Patent Release #1.0, Version #1.25
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/08/748,506
13 FILING DATE: 08-NOV-1996
14 CLASSIFICATION: 435
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 60/033,751
17 FILING DATE: 09-NOV-1995
18 CLASSIFICATION: 435
19 ATTORNEY/AGENT INFORMATION:
20 REFERENCE/DOCKET NUMBER: 74940
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: 312-616-5600
23 TELEFAX: 312-616-5700
24 INFORMATION FOR SEQ ID NO.: 6:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 966 base pairs
27 TYPE: nucleic acid
28 STRANDEDNESS: double
29 TOPOLOGY: linear
30 MOLECULE TYPE: DNA (genomic)
31 US-08-748-506-6
32
33 Alignment Scores:
34 Pred. No.: 4,3e-57 length: 966
35 Score: 574.00 Matches: 121
36 Percent Similarity: 55.8% conservative: 51
37 Best Local Similarity: 39.2% Mismatches: 136
38 Query Match: 35.6% Indels: 0
39 DB: Gaps: 0
40
41 US-09-898-586-24 (1-310) x US-08-748-506-6 (1-966)
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43 QY 3 AspasnIlehrsSerIlehcrluhleuleuenglypheProvalglyproargile 22
44 ::::: |::::| ||||| ||||| |||||
45 Db 28 GAGAAATGATTGTCTGTCAACAGCTTGTCATTTGCCAAGTTCCTGAGGCTCCGGAGAA 87
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47 QY 23 GlmetLeuIleuPhecdyleuPheSerLeuPheThryValPheThrLeuenglyAsnclly 42
48 ::::: |::::| ||||| ||||| ::::: |::::| |||||
49 Db 88 TGTCTCCTCGCTGCACCCCTCATCTCTGTATCTTACTATCACTAACAGAAATGCT 147
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51 QY 43 ThrilleuenglyleuIleSerLeuaspSerArgLeuHisIlaPrometLyrPheheleu 62
52 ::::: |::::| ||||| ||||| ||||| ||||| ||||| |||||
53 Db 148 CTCATACCCTTGCTGNTGTACCAAGTCATCTCTACACACCCTCATGTACTCTTTTG 207
54
55 QY 63 SerhisLeuAlaValAlaSpillealTryAlaCysasnThryValProargmelLeuAl 82
56 ::::: |::::| ||||| ||||| ||||| ||||| ||||| |||||
57 Db 208 GCCAACTTGTCTCTCGAGATGGCTATGCTGTGTACATCCCAAGAATGCTGAG 267
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59 QY 83 AsnleuLeuIsrProblaysrProIleserPhehaIdgLyrgmetcglorhPheleu 102
60 ::::: |::::| ||||| ||||| ||||| ||||| ||||| |||||
61 Db 268 AGCCTTGAGTGAGGCCAGAGATCTCTAGGAGGGATGTCCACACAGATGTTTTTC 327
62
63 QY 103 PheserThrpheAlaValrhglucySleuDeuValValmetserTyraSplreutyr 122
64 ::::: |::::| ||||| ||||| ||||| ||||| ||||| |||||
65 Db 328 TTCACATTTTGTGGCAWACAGAGGCGCATTTAGGCCACCATGCTTGTACCGCTGC 387
66
67 QY 123 ValaIatlecyshisProleuargrtyrLeuAlaIlemerThrrprArgValCysllethr 142
68 ::::: |::::| ||||| ||||| ||||| ||||| ||||| |||||
69 Db 388 ATGGGCAATAGCTCCCACTCACATATGCAACCGGAATGAGTGTAGATGTGCCAT 447
70
71 QY 143 LeuAlaValrhSerTrpThrnglyValleuLeuSerleuIlehisLeuValleu 162
72 ::::: |::::| ||||| ||||| ||||| ||||| ||||| |||||
73 Db 448 TTGCATTTCTTTCATGGGAGTAGGATGCTACTAGTGTGGAGAGCCATTNNAT 507

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Db	88	TTTCCTTCTCTTCGACTATGCTGTGGTGTGACAGAAACATCTCATATAGACA	147
Cy	48	TTleSerLeuAspSerArgLysLeuHisAlaProMetTyrPhePheLeuSerHisLeuAlaVal	67
Db	148	ATTAGAGAACCCACCCACCCCTCCACAAACCCATGATATTTTCTGTGGTAAATATGTCATTT	207
Cy	68	valAspLleAlaIatyrAlaCysAsnThrValPProArgMetLeuValAsnLeu-----	85
Db	208	CTTGAGATTTGGTATGTCATGCTGTTACATTTCTCTAGATGTCGTGGCTGCTCATTTGCC	267
Cy	86	-----HisProAlaLysProLleSerPheAlaGlyArgMetMetClnThrPheLeuPhe	107
Db	268	AAGGACACCATGAGACACTGATCTCTTCTGAGCATGATGACACAACTCATCTTTTTC	327
Cy	104	SerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAspLeuTyrVal	123
Db	328	CTTGCGTGGGTGGCAGAGAGTGTCTCTTCTCTGTATGGCTATGACCCGCTATTTGTG	387
Cy	124	AlAlleCysHisProLeuArgGlyLeuAlaIleMetThrTrrPrArgAlaCysLleThrLeu	144
Db	388	GCTATCTGTCATTCACCTCAGTACCCGCTATTTCTCATGAGCGGGTATGTGGCAGATG	447
Cy	144	AlaValThrSerTrrThrThrGlyValLeuLeuSerLeuLleHisLeuValLeuLeuLeu	166
Db	448	GCACCTGATGCTGGGGCTGGAGGTTTGTATCTGCATCGTTAAAGTTTCTTATTTCT	507
Cy	164	ProLeuProPheCysArgProClnLysLleTyrHisPhePheCysLleLeuAlaVal	187
Db	508	CGCCTGTCTTACTGTGGCCCCAACACATCAACACATTTTCTGTATGTGTCCTCATTG	567
Cy	184	LeuLysLeuLacCysAlaAspPheHisLleAsnGlnAsnMetValLeuAlaGlyAlaIle	207
Db	568	CTCAACCTGTCACTGACCTGATGCATGCCACAGACAGAGCTTTCAGACTTTGCTGGCCATT	627
Cy	204	SerGlyLeuValGlyProLeuSerThrLleValValSerTyrMetCysLleLeuCysAla	227
Db	628	TTTATTCGTGGGAGCGCTCTGTGACCTGGGCGATCTCAACAGCCACACAGAGTCTGT	687
Cy	224	LleLeuGlnLleGlnSerArgLysValGlnArgLysAlaPheCysThrCysPheSerHis	247
Db	668	GTTAGTGGCATCCCTCAGCTGCTGGCCGCCATTAAGCTTTTCACACTGTGCTGCCAC	747
Cy	244	LeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGlyProArgTyr	267
Db	748	CTCACTCTGTGATCATCTTTATGTGACGCCATATTTTCATCTATGCCAGGCTTAAGCA	807
Cy	264	GlyAsnProLysGlnGlnLysTyrLleLeuLeuPheHisSerLeuPheAsnProMet	287
Db	808	CTTCACAGCTTTTGCACACACAAACAGCGTCTGTGACTCTACGCTGCATGTGACCGTTG	867
Cy	284	LeuAsnProLeuLleCysSerLeuArgAsn	293
Db	868	TTTCATCCCATCATCTACTCTGTGCCAC	897
RESULT 10			
US-09-668-680-11			
Sequence 11, Application US/09668680			
Patent No. 6436703			
GENERAL INFORMATION:			
APPLICANT: Tang, Y. Tom			
APPLICANT: Liu, Chenghua			
APPLICANT: Zhou, Ping			
APPLICANT: Asundi, Vinod			
APPLICANT: Zhang, Jie			
APPLICANT: Wang, Jian-Bui			
APPLICANT: Xue, Aidong J.			
APPLICANT: Dimaenac, Radoje T.			
TITLE OF INVENTION: No. 6436703el Nucleic Acids and			
FILE REFERENCE: 790CIP2A			
CURRENT APPLICATION NUMBER: US/09/668,680			
CURRENT FILING DATE: 2000-09-22			

Qy 264 GLYASnProLysGluGlnLysIleuLeuLeuPheHisSerLeuPheAsnProMet 283
Db 811 AGAAGCGAGCTGGACACCAACAGAGGCTGCTTGTCAACATGCTGTGACACCCCTT 870
Qy 284 LeuAsnProLeuLecysSerLeuArgAsnSerGluValIleuAsnThrLeuLysArgVal 303
Db 871 CTGAACCGCTCATCTACACACCCCTGCCACACAGAGGTCCACAGGCTCTCAGGAGTCT 930
Qy 304 Leu 304
Db 931 CTG 933

RESULT 13
US-09-680-13
Sequence 13, Application US/09668680
Patent No. 6436703
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Wang, Jian-Rui
APPLICANT: Xue, Aiqing J.
APPLICANT: Xu, Chongjun
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6436703el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790CIP2A
CURRENT APPLICATION NUMBER: US/09/668,680
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PL-FL-genes Version 2.0
SEQ ID NO 13
LENGTH: 1539
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (130)..(1539)
US-09-680-13

Alignment Scores:
Seq. No.: 8,59e-39 Length: 1539
Score: 418.50 Matches: 96
Percent Similarity: 55.00% Conservative: 58
Best Local Similarity: 34.29% Mismatches: 119
Query Match: 26,018 Indels: 7
DB: 4 Gaps: 3

US-09-898-586-24 (1-310) x US-09-668-680-13 (1-1539)
Qy 30 PheserLeuPheTyValPheThrLeuLeuGlyAsnGlyThrIleLeuGlyLeuLieser 49
Db 682 TTCTGTGCCATGATCTTGTAGACATGCTGTGGAATGCGCCCTCATCTGCTCATTTGCC 741
Qy 50 LeuAspSerArgLeuHisAlaProMetIleuPheLeuSerHisLeuAlaValAlasp 69
Db 742 ATGACAAATCTCTTTCATGACCACTAGTACTCTCTGCTCTCTCTCATCTCACAGAC 801
Qy 70 IleAlaTyAlaCysAsnThrValProArgMetLeuValAsnLeuLeuHisProAlaLys 89
Db 802 CTGCTCTCAGTCTTACCACTGTGCCAAGATGCTGCCATTTTGTGGCTCATCTGCTGT 861
Qy 90 ProLieserPheAlaGlyArgMetMetGlnThrPheLeuPheSerThrPheAlaValThr 109
Db 862 GAGATTCTCTTGTGTGATGCTGTGCCAAGATGTTTGTGTCCATTCATTCATCTCTG 921

Qy 110 GluCysLeuLeuLeuValValMetSerTyTrAspLeuTyValAlaIleCysHisProLeu 129
Db 922 GAGTCTCGATTCTTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 981
Qy 130 ArgTyLeuAlaIleMetThrTrpArgValCysIleThrLeuAlaValThrSerTrpThr 149
Db 982 AGGTATACAAACCATTCATCAACCATCTGTCATAGGCAAGAAATGGCTTGTGGGCTATTC 1041
Qy 150 ThrGlyValLeuLeuSerLeuLeuHisLeuValLeuLeuLeuProLeuProPheCysArg 169
Db 1042 CGTAGTGTGCTATTGTCTCCCTTCATCTCTTGTGCTGAGGAGGAGGAGGAGGAGGAG 1101
Qy 170 ProGlnLysIleTyHisPhePheCysGluIleLeuAlaValLeuLysLeuAlaCysAla 189
Db 1102 CACCGTGTATGACACACACATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1161
Qy 190 AspThrHisIleAsnGluAsnMetValLeuAlaGlyAlaIleSerGlyLeuValGlyPro 209
Db 1162 -----ACATCACTGTCATATTTGCTATGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1215
Qy 210 LeuSerThrIleVal-----ValSerTyMetCysIleLeuCysAlaIleLeuGlnIle 227
Db 1216 CTGATTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCT 1275
Qy 228 GlnSerArgGluValGlnArgLysAlaPheCysThrCysPheSerHisLeuCysValIle 247
Db 1276 CCATTCATGATGCCACACACACATCTGATGATGATGATGATGATGATGATGATGATGAT 1335
Qy 248 GlyLeuPheTyGlyThrAlaIleMetTyValGlyProArgTyGlyAsn----- 265
Db 1336 CTGATTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCT 1395
Qy 266 ---ProLysGluGlnLysIleuLeuLeuPheHisSerLeuPheAsnProMetLeu 284
Db 1396 GTCCCAACAGATGTCACATCTTCTGCTATCTCTATCTGTGCTGTGCTGTGCTGTGCT 1455
Qy 285 AsnProLeuLecysSerLeuArgAsnSerGluValLysAsnThrLeuLysArgValLeu 304
Db 1456 AATCTATTCCTATGAGCTAGAACCAAGAGATTGAGAGTCCAGCTTCATAACTGCTT 1515
RESULT 14
US-09-605-785-526
Sequence 526, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FASTED for Windows Version 3.0
SEQ ID NO 526
LENGTH: 963
TYPE: DNA
ORGANISM: Homo sapiens


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QY 156 LeuIleHisLeuValleuLeuLeuProLeuPheCysArgProGlnIlyHis 175
Db 466 TTGCCACTGCTCTGTGATCAAGGGGCTTCTGCCACTCCATGTCCTCTCGCAC 525
QY 176 PhePheCysGlnIleLeuAlaValleuLysLeuAlaCysAlaAspThrHisIleAsnGlu 195
Db 526 TCCTATTGTCGTCCACCAAGCATGTAATGAAGTGGCTATGCACACACT----- 573
QY 196 AsnMetValleuAlaGlyAlaIleSerGlyLeuValGlyProLeuSerThr----- 212
Db 574 -----TTGCCCAATGTGGTATATGTCCTTACTGCCATTTCCTGTGTCATGGCGCTG 624
QY 213 -----IleValValSerTyrMetCysIleLeuCysAlaIleLeuGlnIleGln 228
Db 625 GACGTATGTTCATCTCTGCTTGTCTATTTTCGTATATACGAACGGTCTGCAACTGGCT 684
QY 229 SerArgGluValGlnArgLysAlaPheCysThrCysPheSerHisLeuCysValIleGly 248
Db 685 TCCAACTCAGAGCGGCCCAAGGCTTTGGAACTGTGTGTACACATTTGGTGTACTC 744
QY 249 LeuPheTyrGlyThrAlaIleIleMetTyrValGlyProArgTyrGlyAsnProLysGlu 268
Db 745 GCCTTCATGTGCACACTTATGTGGCTCTCAGTTGTACACCGCTTGGAAACACGCTTCAT 804
QY 269 GlnLysLysTyrLeuLeuLeu-----PheHisSerLeuPheAsnProMetLeuAsnPro 286
Db 805 CCCATTGTGCGTGTGTTCATGGGTGACATCTACCTGTGCTGCTCCTGTGTCATCAATCCC 864
QY 287 IleuIleCysSerLeuArgAsnSerGluValLysAsnThrLeuLysArgValleuGlyVal 306
Db 865 ATCATCTATGTGTCCAAACCAACACAGATCAGAACCA-----CGGCTGCTGGCTATG 915
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Search completed: January 2, 2003, 09:09:48
Job time : 85 secs

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•

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 2, 2003, 08:42:37 ; Search time 805 Seconds
(without alignments)
166.554 Million cell updates/sec

Title: US-09-898-586-24

Perfected score: 1609
Sequence: 1 MGDNTSITEFLLGFPVGP.....LRNSEVKNLKLRLVGERAL 310

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 381593 seqs, 216252194 residues

Total number of hits satisfying chosen parameters: 763186

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database: PublishedApplications_NA.*

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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1609	100.0	1012	10	US-09-761-288-21
2	1584	98.4	1040	10	US-09-761-288-3
3	1584	98.4	1040	10	US-09-761-288-34
4	1568	97.5	1014	10	US-09-761-288-23

ALIGNMENTS

RESULT 1
US-09-761-288-21
Sequence 21, Application US/09761288
Patient No. US20020065405A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Mutalidhara
APPLICANT: Prayaga, Sudhirdas
APPLICANT: Raupier, Raymond J
APPLICANT: Mishra, Vishnu
APPLICANT: Tchernev, Valtzar
APPLICANT: Spytek, Kimberky
APPLICANT: Li, Li
TITLE OF INVENTION: NO. US20020065405A1el Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: 15966-638
CURRENT APPLICATION NUMBER: US/09/761,288
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/177,839
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/176,134
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/175,989
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: 60/218,324
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/220,253
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/178,191
PRIOR FILING DATE: 2000-01-26

5	1147	71.3	2282	9	US-10-098-841-92	Sequence 92, Appl
6	1147	71.3	2282	10	US-09-747-835A-62	Sequence 62, Appl
7	1138	70.7	1788	10	US-09-747-835A-35	Sequence 35, Appl
8	1138	70.7	2735	10	US-09-747-835A-34	Sequence 34, Appl
9	1126	70.0	933	10	US-09-864-761-30527	Sequence 30527, A
10	1126	70.0	1957	10	US-09-864-761-13963	Sequence 13963, A
11	1080	67.1	927	10	US-09-747-835A-41	Sequence 41, Appl
12	1080	67.1	1782	10	US-09-886-055-484	Sequence 484, Appl
13	991	61.6	933	10	US-09-886-055-472	Sequence 472, Appl
14	947.5	58.9	930	10	US-09-886-055-486	Sequence 486, Appl
15	930	57.8	933	10	US-09-886-055-482	Sequence 482, Appl
16	881	54.8	936	10	US-09-812-102-72	Sequence 72, Appl
17	790	49.1	456	10	US-09-886-055-440	Sequence 440, Appl
18	692	43.0	939	10	US-09-886-055-452	Sequence 452, Appl
19	670.5	41.7	936	10	US-09-886-055-452	Sequence 452, Appl
20	670	41.6	1008	10	US-09-886-055-200	Sequence 200, Appl
21	669	41.6	942	10	US-09-886-055-398	Sequence 398, Appl
22	668	41.6	957	10	US-09-886-055-315	Sequence 315, Appl
23	668	41.5	939	10	US-09-886-055-326	Sequence 326, Appl
24	666	41.4	932	9	US-10-032-106-2	Sequence 2, Appl
25	666	41.4	949	10	US-09-755-017-1	Sequence 1, Appl
26	666	41.4	1488	10	US-09-755-017-3	Sequence 3, Appl
27	661.5	41.1	995	10	US-09-771-730-31	Sequence 31, Appl
28	661	41.1	1053	10	US-09-886-055-398	Sequence 398, Appl
29	660.5	41.1	930	10	US-09-771-730-110	Sequence 110, Appl
30	660.5	41.1	993	10	US-09-886-055-200	Sequence 200, Appl
31	660.5	41.1	994	10	US-09-771-730-23	Sequence 23, Appl
32	660	41.0	951	10	US-09-886-055-180	Sequence 180, Appl
33	659.5	41.0	921	10	US-09-771-730-135	Sequence 135, Appl
34	659.5	41.0	960	10	US-09-771-730-35	Sequence 35, Appl
35	659.5	41.0	968	10	US-09-771-730-139	Sequence 139, Appl
36	659.5	41.0	994	10	US-09-771-730-134	Sequence 134, Appl
37	658.5	40.9	921	10	US-09-771-730-25	Sequence 25, Appl
38	658.5	40.9	994	10	US-09-771-730-33	Sequence 33, Appl
39	658.5	40.9	994	10	US-09-886-055-138	Sequence 138, Appl
40	658.5	40.8	994	10	US-09-886-055-326	Sequence 326, Appl
41	656	40.8	1954	10	US-09-864-761-5098	Sequence 5098, Appl
42	656	40.7	930	10	US-09-771-730-111	Sequence 111, Appl
43	655.5	40.7	975	10	US-09-886-055-498	Sequence 498, Appl
44	653	40.6	975	10	US-09-886-055-466	Sequence 466, Appl
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; PRIOR APPLICATION NUMBER: 60/178,227
 ; PRIOR FILING DATE: 2000-01-26
 ; PRIOR APPLICATION NUMBER: 60/220,590
 ; PRIOR FILING DATE: 2000-07-25
 ; NUMBER OF SEQ ID NOS: 95
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 21
 ; LENGTH: 1012
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-761-288-21

Alignment Scores:
 Pred. No.: 2,76e-163 Length: 1012
 Score: 1609.00 Matches: 310
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-898-586-24 (1-310) x US-09-761-288-21 (1-1012)

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|||||
21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyValPheThrLeuLeuGly 40
|||||
114 AGGATTCAGATGCTCTCTTGGGCTCTTCCCTGCTTCTACGTTCTTACACCTGCTGGG 173
|||||
41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyPhe 60
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174 AACGGAGCAATACTGGGGCTCATCTCAGGACTCCAGACTGACGCCCATGACTATCTC 233
|||||
61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyAlaCysAsnThrValProArgMet 80
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234 TTCCTCTACACCTGGCGGCTGCGACATCGCCTACGCCCTGCACACGATGCCCGCATG 293
|||||
81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetGlnThr 100
|||||
294 CTGGTAGACCTCTGTCATCAGCAAGCCCATCTCTTGGGGCGCGCATGACAGACC 353
|||||
101 PheLeuPheSerThrPheAlaValThrGlyCysLeuLeuValValMetSerTyTrasp 120
|||||
354 TTTCTGTCTTTCACCTTTGCTGTCACAGAAATGCTCTCTGCTGGTGTGATGCTCATGAT 413
|||||
121 LeuTyValAlaIleCysHisProLeuArgTyLeuAlaIleMetThrTrpArgValCys 140
|||||
414 CTGTACGTGGCCATCTGCCACCCCTCCGATATTGGCCATCATGACCTGGAGACTGTC 473
|||||
141 IleThrLeuAlaValThrSerTrpThrTrpThrGlyValLeuLeuSerLeuIleHisLeuVal 160
|||||
474 ATCACCTCGCGGTGACTTCTGAGCACTGAGACCTGATCTTTATCTTCAATCTTGTG 533
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161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyHisPhePheCysGluIle 180
|||||
534 TTACTTCTTACCTTTACCTCTGTGAGCCCAAGAAATTTATCACTTTTGTGAAATTC 593
|||||
181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGlnAspMetValLeuAla 200
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594 TTGGCTGTCTCAAACTTCGCTGTGCAGATACCAATCAATGAGAACATGCTGTGCC 653
|||||
201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyMetCysAla 220
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654 GGAGCAATTTCTGGCTGGTGGACCTTGTGCACAAATTTGATTTCAATATGAGCATC 713
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221 LeuCysAlaIleLeuGlnIleGlnSerArgIleValGlnArgLysAlaPheCysThrCys 240
|||||
714 CTCTGTGCTATCTTCAATCCAAATCAAGGAAATTCAGAGAAAGCCCTTGTGCCCTGC 773
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281 AsnProMetLeuAsnProLeuIleCysSerLeuAlaGlnSerGlyValLysAsnThrLeu 300
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894 AATCCCATGCTCATCTCCCTTATGCTGTAGCTCTTACGAACTCAGAAATATCACTTGG 953
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RESULT 2

US-09-761-288-3
 ; Sequence 3, Application US/09761288
 ; Patent No. US20020065405A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Padigar, Murallidhara
 ; APPLICANT: Prayaga, Sudhirdas
 ; APPLICANT: Taupier, Raymond J
 ; APPLICANT: Mishra, Vishnu
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Li, Li
 ; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding
 ; FILE REFERENCE: 15966-638
 ; CURRENT APPLICATION NUMBER: US/09/761,288
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: 60/177,839
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: 60/176,134
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: 60/175,989
 ; PRIOR FILING DATE: 2000-01-13
 ; PRIOR APPLICATION NUMBER: 60/218,324
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 60/220,253
 ; PRIOR FILING DATE: 2000-07-24
 ; PRIOR APPLICATION NUMBER: 60/178,191
 ; PRIOR FILING DATE: 2000-01-26
 ; PRIOR APPLICATION NUMBER: 60/178,227
 ; PRIOR FILING DATE: 2000-01-26
 ; PRIOR APPLICATION NUMBER: 60/220,590
 ; PRIOR FILING DATE: 2000-07-25
 ; NUMBER OF SEQ ID NOS: 95
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 1040
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-761-288-3

Alignment Scores:

Pred. No.: 1.36e-160 Length: 1040
 Score: 1584.00 Matches: 307
 Percent Similarity: 99.03% Conservative: 0
 Best Local Similarity: 99.03% Mismatches: 3
 Query Match: 98.45% Indels: 0
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US-09-898-586-24 (1-310) x US-09-761-288-3 (1-1040)

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21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyValPheThrLeuLeuGly 40
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142 AGGATTCAGATGCTCTCTTGGGCTCTTCCCTGCTTCTACGTTCTTACCTGCTGGG 201
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41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyPhe 60
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Db 262 TTCCTCTACACCTGGGGGTGGTGGACATGCTGACCGCTGGCAACGAGGGCCCGGATG 321
Qy 81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetGlnThr 100
Db 322 CTGGTGAACCTCCCTGCATCCAGGCCAACGCCATCTCTTCGCGGGCCGATGATGAGACC 381
Qy 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAsp 120
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Qy 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCys 140
Db 442 CTGTACGCGGCGCATCTGCCACCCCTCCGATATTGGCCATCATGACCTGGAGAGCTCCG 501
Db 141 IlePheLeuAlaValThrSerTrpThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 502 ATCACCCCTCGGCGTACCTCTCGACCCACCTGAGCCCTTTATCTTATCTTGATCTCTTGTG 561
Qy 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
Db 562 TTACTTCTACCTTACCCCTCTCTGAGGCCCCAGAAATTTATCATCTTTTGTGAATTC 621
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Qy 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
Db 682 GGAGCAATTTCTGGCGTGGTGGGACCTGTCCACAAATTGATTTCAATATATGTCATTC 741
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Qy 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
Db 802 TTCCTCCACCTCTGTGATGATGACCTGTATGTCACACCCATTTATCATGTTATGTGGA 861
Qy 261 ProArgTyrGlyAsnProLysGlnGlnLysTyrLeuLeuLeuPheHisSerLeuPhe 280
Db 862 CCCAGATATGGGAACCCCAAGAGACAGAAATATATCTCTGCTGTTTTCAGACCTCTTT 921
Qy 281 AsnProMetLeuAsnProLeuIleCysSerLeuArgHisSerGluValLysAsnThrLeu 300
Db 922 AATCCCACTCAATCCCTTATCTGATGCTTAGGAACTCAGAAAGTGAATACTTTG 981
Qy 301 LysArgValLeuGlyValGluArgAlaLeu 310
Db 982 AAGAGAGTCTGGAGTATGAAGAGGCTTTA 1011

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; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-34
Alignment Scores:
Pred. No.: 1,366-160 Length: 1040
Score: 1584.00 Matches: 307
Percent Similarity: 99.03% Conservative: 0
Best local Similarity: 99.03% Mismatches: 3
Query Match: 98.45% Indels: 0
Dbs: 10 Gaps: 0
US-09-898-586-24 (1-310) x US-09-761-288-34 (1-1040)
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Qy 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuGly 40
Db 142 AGGATTCAGATGCTCCCTTTGGGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 201
Qy 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhe 60
Db 202 AACGGGACCAATCTGGGCGTCACTGACTGACTGACTGACTGACTGACTGACTGACTG 261
Qy 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
Db 262 TTCCTCTACACCTGGGGGTGGTGGACATGCTGACCGCTGGCAACGAGTGGCCGATG 321
Qy 81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyArgMetGlnThr 100
Db 322 CTGGTGAACCTCCCTGCATCCAGGCCAACGCCATCTCTTCGCGGGCCGATGATGAGACC 381
Qy 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAsp 120
Db 382 TTCCTGTTTCCACTTTTGGTGTGACGAAATGTCCTCTCGTGGTGGTGGATGCTTAATG 441
Qy 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCys 140
Db 442 CTGTACGCGGCGCATCTGCCACCCCTCCGATATTGGCCATCATGACCTGGAGAGCTCC 501
Qy 141 IlePheLeuAlaValThrSerTrpThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 502 ATCACCCCTCGGCGTACCTCTCGACCCACCTGAGCCCTTTATCTTATCTTGATCTCTTGT 561
Qy 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
Db 562 TTACTTCTACCTTACCCCTCTCTGAGGCCCCAGAAATTTATCATCTTTTGTGAATTC 621
Qy 181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
Db 622 TTGGCTGTCTCAAACTTGCTGTGACGATGCCACATCAATGAAGACATGAGTGGCTGG 681
Qy 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220

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RESULT 3

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US-09-761-288-34
; Sequence 34, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Vellizar
; APPLICANT: Spytek, Kimberly
; TITLE OF INVENTION: No. US20020065405A1el polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: 60/177,939
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134

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Db 682 GGAGCAATTCTGGGCTGGTGGGACCCCTGTCCACAATTGATTGATATATGTGCATC 741
Qy 221 LeucysAlaIleleuGlnIleGlnSerArgIuValGlnArgIysAlaIaPheCysThrCys 240
Db 742 CTCGTCTCTATCTCTTCAGATCCATCAAGGAGGATTCAGAGAAAGCCTTCGACCTGC 801
Qy 241 PheSerHisLeucysValIleGlyLeuPheTyrglyThrAlaIleIleMetTyrgly 260
Db 802 TTCCTCCACCTCTGTGTGATGGATGCCTGTTATGGCACAGCCATTATCATGTATGTTGA 861
Qy 261 ProArgTyrglyAsnProIysGlnGlnIlystTyrlleuLeuPheHisSerLeuPhe 280
Db 862 CCCAGATATGGAAACCCAGAGGAGCAGAGAAATATCTCTGCTTTCAACAGCCTCTT 921
Qy 281 AsnProMetLeuAsnProIleuIleCysSerLeuArgAsnSerGluValIysAsnThrLeu 300
Db 922 AATCCCATGCTCAATGCCCTTATCTGTACTGTAGTAAGCTCGAAGTGAACATACCTTG 981
Qy 301 LysArgValIleuGlyValGluArgAlaLeu 310
Db 982 AAGAGAGTGGCTGGAGAGAAAGGCTTTA 1011
SUBT 4
US-09-761-288-23
; Sequence 23, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OR INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
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; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-23
Alignment Scores:
Pred. No.: 6,79e-159 Length: 1014
Score: 1568.00 Matches: 309
Percent Similarity: 99.36% Conservative: 0
Best Local Similarity: 97.36% Mismatches: 1
Query Match: 97.45% Indels: 2
DB: 10 Gaps: 0
US-09-898-586-24 (1-310) x US-09-761-288-23 (1-1014)
Qy 1 MetGlyAspAsnIleThrSerIleThrGlnPheLeuLeuGlyPheProValGlyPro 20

Lb 55 ATGGGGGACAAATATATACATTCACATCACAGATGTCCTCTACTGGAGTTCCGGTGGCCCA 114
Cy 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrglyValPheThrLeuLeuGly 40
Lb 115 AGCATTCAGATGCTCCCTTTGGGCTCTTCCCTGTTTACGTCCTTACCCCTGCTGGGG 174
Cy 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrgly 60
Lb 175 AACGGAGCACATACGGGGGCTCATTCAGAGACTCCAGACTGCAGCCCTCG-TRACTTC 233
Qy 61 PheLeuSerHisLeuAlaValIleAspIleAlaTyrglyAlaCysAsnThrValProArgMet 80
Lb 234 TTCCTCTACACCTCGCGCTGTGCATACGCTACGCTCGCAACACGCTCCCGCATG 293
Qy 81 LeuValAsnLeuLeuHisProAlaIysProIleSerPheAlaGlyArgMetLeuThr 100
Lb 294 CTGGTGAACCTCTCGCATCCAGCAGCCATCTCTTTGGGGCCGATGATGCAGACC 353
Qy 101 PheLeuPheSerThrPheAlaValThrGlnCysLeuLeuValValMetSerTyrgly 120
Lb 354 TTCGTGTTTCACCTTTTGCTGTGCAGAGATGCTCTCTGTGTGTGTGTGTGTGTGTGTGT 413
Qy 121 LeuTyrglyAlaIleCysHisProLeuArgTyrlleuAlaIleMetThrTrpArgValCys 140
Lb 414 CTGTACGTGGCCATCTGCCACCCCTCCGATATTTGGCATATGACCTGGAGACTCTGC 473
Qy 141 IleThrLeuAlaValThrSerTrpThrGlyValIleLeuSerLeuIleHisLeuVal 160
Lb 474 ATCAACCTCGCGGTGACTCTCTGGACACAGTGCAGTCTTTATCTGTGATCATCTGTG 533
Qy 161 LeuLeuLeuProLeuProPheCysArgProGlnIysIleTyrlHis-PhePheCysGluIle 180
Lb 534 TTACTCTACCTTTACCTCTGTAGGCCCCAGAAATTTATCATTCTTTTGTGAAAT 593
Qy 180 LeuAlaValLeuLeuLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAl 200
Lb 594 CTGGCTGCTTCYCAACTTCCTGTGTGAGATACCCACATCAAGAAACATGCTGTGGC 653
Qy 200 AglyAlaIleSerGlyLeuValGlyProLeuSerThrIleValIleSerTyrglyMetCysIle 220
Lb 654 CGAGCAATTTCTGGCTGTGGGACCTTGTCACAAATTTGAGTTGATATATGTGCAT 713
Qy 220 LeucysAlaIleleuGlnIleGlnSerArgIuValGlnArgIysAlaIaPheCysThrCys 240
Lb 714 CCTGTGCTCTATCTCTCAGATCCATCAAGGAGTTCAGAGAAAGCCTTCGCACCTG 773
Qy 240 sPheSerHisLeucysValIleGlyLeuPheTyrglyThrAlaIleIleMetTyrgly 260
Lb 774 CTCCTCCACCTCTGTGTGATGGACTCTTTATGGCACAGCCATTATCATGTATGTTGG 833
Qy 260 yProArgTyrglyAsnProIysGlnGlnIlystTyrlleuLeuPheHisSerLeuPhe 280
Lb 834 ACCCGATATGGAAACCCCAAGGAGCAGAGAAATATCTCTGCTTTCAACAGCCTCTT 893
Qy 280 eAsnProMetLeuAsnProIleuIleCysSerLeuArgAsnSerGluValIysAsnThrLe 300
Lb 894 TAATCCATGCTCAATCCCTTATCTGTAGTCTAGGAAGCTCGAAGTGAACATACCTTT 953
Qy 300 LysArgValIleuGlyValGluArgAlaLeu 310
Lb 954 GAGAGAGTGGCTGGAGAGAAAGGCTTTA 984
RESULT 5
US-10-098-841-92
; Sequence 92, Application US/10098841
; Publication No. US20020197679A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping


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Db 725 TGGTGAACCTCCGATCCAGCCAGCCCATCTCTTGGCGGATGACATAGACC 784
Qy 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAsp 120
Db 785 TTTCTCTTTTGGATTGACATGACTGGAATGCTCTCTGTGTGCTGATGCTTACGAT 844
Qy 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCys 140
Db 845 CGGTACGTGGGCATCTGCCACCTCTCCGATATTTCATCATCATGACCGGAAAGCTCTCC 904
Qy 141 IleThrLeuAlaValThrSerTyrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 905 ATCACTGTGGCCATCACTCTCTGACATGTGGCTCCCTCTGCTGTGTGCTCATCTTTGCA 964
Qy 161 LeuLeuLeuProLeuProPheCysArgProGluLysIleTyrHisPhePheCysGluIle 180
965 CTCATCTCAAGACTGCCCCCTTTGTGGGCTCTGGAATCAACCACTTCTTCTGTAATC 1024
181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
Db 1025 CTGTCCTCTCTCAAGCGGCGCTGTGCTGATCACTGCTCAACCAAGGTGCTCATCTTTGCA 1084
Qy 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
Db 1085 GCCGTGATGTTTCATCTCGTGGGAGGACCACTCTGCTGTGCTCTCTCTACACACATC 1144
Qy 221 LeuCysAlaIleLeuGluIleGlnSerArgGluValGlnArgLysAlaPheCysThrCys 240
Db 1145 CTGGCGGCGATCCCTGAGGATCCAGTCTGGGAGGCGGCGGCGGCGGCGGCGGCGGCGG 1204
Qy 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
Db 1205 TCCGTCACCTCTCTCGTGGGAGGAGCTTCTTGGCAGCCCACTCTCTCTCTCTCTCTCT 1264
Qy 261 ProArgTyrGlyAsnProLysGluGlnLysLysTyrLeuLeuPheHisSerLeuPhe 280
Db 1265 CCTAAGTCCCGCCATCTCTGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1324
Qy 281 AsnProMetLeuAsnProLeuIleCysSerLeuArgAsnSerGlyValLysAsnThrLeu 300
Db 1325 AACCCGATGCTAAACCCCTGATTTACACCTGAGCAAGTAAGTAGAGTCAAGGGTGGCTG 1384
Qy 301 LysArgValLeu 304
Db 1385 AGGAGAGCAGCTG 1396

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SUBT 8
US-09-747-835A-34
Sequence 34, Application US/09747835A
Patent No. US20020146692A1
GENERAL INFORMATION:
APPLICANT: Yamazaki, Victoria
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Wang, Duntui
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyun
APPLICANT: Asundi, Vinod
APPLICANT: Dimahe, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
FILE REFERENCE: HYS-37C1P
CURRENT APPLICATION NUMBER: US/09/747,835A
PRIORITY APPLICATION NUMBER: US 09/729,739
PRIORITY FILING DATE: 2000-12-04
PRIORITY APPLICATION NUMBER: US 09/653,450
PRIORITY FILING DATE: 2000-08-31
PRIORITY APPLICATION NUMBER: US 09/620,312
PRIORITY FILING DATE: 2000-07-19
PRIORITY APPLICATION NUMBER: US 09/598,042

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; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 2735
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-747-835A-34
Alignment Scores:
Pred. No.: 3,12e-112 Length: 2735
Score: 1138.00 Matches: 219
Percent Similarity: 84.54% Conservative: 38
Best Local Similarity: 72.04% Mismatches: 47
Query Match: 70.73% Indels: 0
DB: Gaps: 0
US-09-898-586-24 (1-310) x US-09-747-835A-34 (1-2735)
Qy 1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyPro 20
Db 1335 ATGTGAAATATCAGACATAGTCACAGAGTTCTCTACTGGGATTTCTCTGGGCCCA 1394
Qy 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuGly 40
Db 1395 AGGATTCAGATGCTCTCTTGGGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1454
Qy 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuIleAlaProMetTyrPhe 60
Db 1455 AATGGACCATCTCGGGGCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1514
Qy 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
Db 1515 TTCTCTCAACACGCGCGCTGCTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1574
Qy 81 LeuValAsnLeuLeuIleProAlaLysProIleSerPheAlaGlyArgMetMetGlnThr 100
Db 1575 CTGGTGAACCTCTCGATCCAGCCAGCCAGCCAGCTCTTGTGTGGTGGTGGTGGTGGT 1634
Qy 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAsp 120
Db 1635 TTTCTCTTTTGGATTGACATGACTGGAATGCTCTCTGTGTGCTGATGCTTACGAT 1694
Qy 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTrpArgValCys 140
Db 1695 CGGTACGTGGGCATCTGCCACCTCTCCGATATTTCATCATCATGACCGGAAAGTCTCC 1754
Qy 141 IleThrLeuAlaValThrSerTyrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 1755 ATCACTGTGGCCATCACTCTCTGACATGTGGCTCCCTCTGCTGTGCTGCTGCTGCTG 1814
Qy 161 LeuLeuLeuProLeuProPheCysArgProGluLysIleTyrHisPhePheCysGluIle 180
Db 1815 CTCACTCTAAGACTGCCCTTTGTGGGCTCTGGAATCAACCACTTCTTGTGTGGAATC 1874
Qy 181 LeuAlaValLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
Db 1875 CTGTCTGTCCGACGCGCTGTGGTGTGATCTGCTCAACCAAGGTGCTCATCTTTGCA 1934
Qy 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
Db 1935 GCCGTGATGTTTCATCTCGTGGGAGGACCACTGCTGTGCTGCTGCTGCTGCTGCTGCTG 1994
Qy 221 LeuCysAlaIleLeuGluIleGlnSerArgGluValGlnArgLysAlaPheCysThrCys 240
Db 1995 CTGGCGGCGATCCCTGAGGATCCAGTCTGGGAGGCGGCGGCGGCGGCGGCGGCGGCGG 2054
Qy 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260

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Db 2055 TCCTCCACCTCTGCGAGTGGAGACTCTTTGGCAGGCCAGTCATGATGACC 2114
 Oy 261 ProArgTyrIAsnProLysGluGlnLysIAsnTyrLeuLeuLeuPheHisSerLeuPhe 280
 Db 2115 CCGTAGCCCGCATCTGAGGAGCAGAGGTCCTTTCTATTTTACAGTTCTTTC 2174
 Oy 281 AsnProMetLeuAsnProLeuIleCysSerLeuArgAsnSerGluValLysAsnThrLeu 300
 Db 2175 AACCCGATGCTAAACCCCTGATTTCACACCTGAGAGATGTAGAGTCACGGTCGCCCTG 2234

Oy 301 LysArgValLeu 304
 Db 2235 AGGAGACACTG 2246

RESULT 9

US-09-864-761-30527/c
 Sequence 30527, Application US/09864761
 Patent No. US20020048763A1

GENERAL INFORMATION:
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aemica-x-1
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 30527

LENGTH: 933
 TYPE: DNA
 ORGANISM: Homo sapiens

FEATURE:
 OTHER INFORMATION: MAP TO AC004889.1
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.93
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
 OTHER INFORMATION: SWISSPROT HIT: P34964, EVALUATE 1.00e-86
 OTHER INFORMATION: EST_HUMAN HIT: BF16115.1, EVALUATE 0.00e+00
 OTHER INFORMATION: NT HIT: 086281.1, EVALUATE 0.00e+00
 US-09-864-761-30527

Alignment Scores:

Pred. No.:	1,28e-111	Length:	933
Score:	1126.00	Matches:	219
Percent Similarity:	82.08%	Conservative:	33
Best Local Similarity:	71.34%	Mismatches:	55
Query Match:	69.98%	Indels:	0
DB:	10	Gaps:	0

US-09-898-586-24 (1-310) x US-09-864-761-30527 (1-933)

Oy 1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuLeuGlyPheProValGlyPro 20
 Db 930 ATGGGGGAAATACAGACATATGTCACAGAGTTCTCTACTGGATTCTCTCGGGGCCCA 871
 Oy 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuLeuGly 40
 Db 870 AGGATTGAGATGCTCTCTTTGGGCTCTTCCCTGTATATCTTACACCTGCTGGGG 811
 Oy 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhe 60
 Db 810 AACGGGGGACATCGGGGCTCATCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTC 751
 Oy 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
 Db 750 TTCCCTCAGACATCGGCTGTCGTCAGATGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 691
 Oy 81 LeuValAsnLeuLeuHisProAlaLysProIleSerPheAlaGlyAlaMetMetIleThr 100
 Db 690 CTGGGAGACCTCTGCTGATCCAGCCAGCCAGCTCTCTTCTGCTGCTGCTGCTGCTGCTG 631
 Oy 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuLeuValAlaMetSerTyrAsp 120
 Db 630 TTTCTCTGTTTGGACACAGCAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 571
 Oy 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTyrPheValCys 140
 Db 570 CGTTACGCGGCATCTGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 511
 Oy 141 IleThrLeuAlaValThrSerThrThrGlyValIleLeuLeuSerLeuIleHisLeuVal 160
 Db 510 ATCACCCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 451
 Oy 161 LeuLeuLeuProLeuProPheCysArgProGlnLysIleTyrHisPhePheCysGluIle 180
 Db 450 CTCATCTTAAGACGCTCTCTCTGCGCTCAGCAATGCAATGCAATGCAATGCAATGCAATG 391
 Oy 181 LeuAlaValIleLysLeuAlaCysAlaAspThrHisIleAsnGlnLysAsnMetValLeuAla 200
 Db 390 CTGTGCTGCTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 331
 Oy 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
 Db 330 GCTGCGGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 271
 Oy 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgLysAlaPheCysThrCys 240
 Db 270 CTGGCGGCATCTGAGAGATCCAGTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 211
 Oy 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
 Db 210 TCCTGCCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 151
 Oy 261 ProArgTyrGlyAsnProLysGluGlnLysLysTyrLeuLeuLeuPheHisSerLeuPhe 280

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Db 150 CCCAAGTCCGCCATCTGAGGACACCAAGCTCTTTTCTATTTACAGTTTTC 91
Oy 281 AsnProMetLeuAnProLeuIleCysSerLeuArgAsnSerGluValIysAsnThrLeu 300
Db 90 AACCAACACTTAACCCCTGATTTACAGCTGAGGACGAGAGAGTCAAGGGTGCCTG 31
Oy 301 LysArgValLeuGlyValGlu 307
Db 30 AGGAGAGCAGCTGGCGAAGAA 10

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RESULT 10

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US-09-864-761-13963/C
; Sequence 13963, Application us/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

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; APPLICANT: Penn, Sharon G.

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; APPLICANT: Hanzel, David R.

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; APPLICANT: Chen, Wensheng

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; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1

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; CURRENT APPLICATION NUMBER: US-09/864,761

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; PRIOR APPLICATION NUMBER: US 60/180,312

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; PRIOR FILING DATE: 2000-02-04

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; PRIOR APPLICATION NUMBER: US 60/207,456

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; PRIOR FILING DATE: 2000-05-26

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; PRIOR APPLICATION NUMBER: US 09/632,366

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; PRIOR FILING DATE: 2000-08-03

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; PRIOR APPLICATION NUMBER: GB 24263.6

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; PRIOR FILING DATE: 2000-10-04

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; PRIOR APPLICATION NUMBER: US 60/236,359

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; PRIOR FILING DATE: 2000-09-27

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; PRIOR APPLICATION NUMBER: PCT/US01/00666

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; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00667

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; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00664

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; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00669

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; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00665

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; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00668

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; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00670

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; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: US 60/234,687

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; PRIOR FILING DATE: 2000-09-21

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; PRIOR APPLICATION NUMBER: US 09/608,408

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; PRIOR FILING DATE: 2000-06-30

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; PRIOR APPLICATION NUMBER: US 09/774,203

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; PRIOR FILING DATE: 2001-01-29

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; NUMBER OF SEQ ID NOS: 49117

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; SOFTWARE: Annumax Sequence Listing Engine vers. 1.1

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; SEQ ID NO 13963

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; LENGTH: 1957

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; TYPE: DNA

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; ORGANISM: Homo sapiens

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; FEATURE:

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; OTHER INFORMATION: MAP TO AC004889.1

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; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1

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; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1

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; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.93

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; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

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; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
US-09-864-761-13963

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Alignment Scores:

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Prod. No.: 3 72e-111 length: 1957
Score: 1126.00 Matches: 219
Percent Similarity: 82.08 Conservative: 33
Best Local Similarity: 71.34 Mismatches: 55
Query Match: 69.98 Indels: 0
DB: 10 Gaps: 0

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US-09-898-586-24 (1-310) x US-09-864-761-13963 (1-1957)

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Oy 1 MercGlyspasnIleThrSerIleThrGluPheLeuLeuGlyPheProValGlyPro 20
Db 1054 ATGGGGGAAATGACACATGTCACAGAGTCTCTCTGAGATTCCTCTGGGCCCA 995
Oy 21 ArgIleGluMetLeuPheGlyLeuPheSerLeuPheValPheThrLeuLeuGly 40
Db 994 AGATTGATGATGCTCTTGGGCTCTTCCCTCTTATATCTTACCCCTGCGGG 935
Oy 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetThrPhe 60
Db 934 AACGGGCCATCTGGGGCTCATCTCAGACATCCAGACCCCAACCCATGATCTTC 875
Oy 61 PheLeuSerHisLeuAlaValAspIleAlaTyraIysAsnThrValProArgMet 80
Db 874 TTCTCTCACACCTGCTGCTGCGACATCGCTACACCCGACACACGATGCCCATG 815
Oy 81 LeuValAsnLeuLeuHisProAlaIysProIleSerPheAlaGlyArgMetGlnThr 100
Db 814 CTGGGCAACCTCTGCTGATCCAGCAGCCATCTCTTGGCTGGTGCATGACAGACC 755
Oy 101 PheLeuPheSerThrPheAlaValThrGlyCysLeuLeuLeuValValMetSerTyraSp 120
Db 754 TTCTCTGTTGAGTTTGGACACAGCATGCTCTGCTGCTGATGATGCTTACAT 695
Oy 121 LeuTyValAlaIleCysHisProLeuArgTyraIleAlaIleMetThrTrpArgValCys 140
Db 694 CGTTAGCTGGCCATGTCGCCACCTCTCCGATACCTCGCATCATGACCTGGAGATGCG 635
Oy 141 IleThrIleuAlaValIleThrSerThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
Db 634 ATCACCTGGCCGCTGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 575
Oy 161 LeuLeuLeuProLeuPheProPheCysArgProGlnIysIleTyraHisPhePheCysGluIle 180
Db 574 CTGATCTTAAGACTGCGCTCTGCTGCGCTCATGAATCAACACTTCTTGTGAATTC 515
Oy 181 LeuAlaValIleuIysLeuAlaCysAlaAspThrHisIleAsnGlnAsnMetValLeuAla 200
Db 514 CTGCTCTCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 455
Oy 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyraMetCysIle 220
Db 454 GCTGCGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 395
Oy 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgValAlaPheCysThrCys 240
Db 394 CTGGGGCCATCTGAGGATCCAGTCTGGGAGGGCCGAGAAAGCCTTCTCCACCTGC 335
Oy 241 PheSerHisLeuCysValIleGlyLeuPheTyrglyThrAlaIleIleMetTyraValGly 260
Db 334 TCTCCCACTCTGCGTGGGAGGAGCTCTTGTGAGGAGCATCATGATGATGATGAGCC 275
Oy 261 ProArgTyrglyAsnProLysGlnGlnIlyValTyraLeuLeuLeuPheHisSerLeuPhe 280
Db 274 CCCAAGTCCGCCATCTGAGGAGGAGCAAGAGTCTTTTCTATTATACAGTTTTC 215
Oy 281 AsnProMetLeuAnProLeuIleCysSerLeuArgAsnSerGluValIysAsnThrLeu 300
Db 214 AACCAACACTTAACCCCTGATTTACAGCTGAGGACGAGAGTCAAGGGTGCCTG 155

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QY 301 LysArgValIleuGlyValGlu 307
 DB 154 AGGAGGACACTGGCGCAGGAA 134

RESULT 11

US-09-747-835A-43
 : Sequence 43, Application US/09747835A

: Patent No. US2002014692A1
 : GENERAL INFORMATION:

: APPLICANT: Yamazaki, Victoria
 : APPLICANT: Tang, Y. Tom

: APPLICANT: Liu, Chenghua
 : APPLICANT: Zhou, Ping

: APPLICANT: Wang, Dunrui
 : APPLICANT: Zhang, Jie

: APPLICANT: Ren, Feiyun
 : APPLICANT: Asundi, Vinod

: APPLICANT: Drmanac, Radoje T
 : TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE

: FILE REFERENCE: HYS-37CIP
 : POLYPEPTIDES AND POLYNUCLEOTIDES

: CURRENT APPLICATION NUMBER: US/09/747, 835A
 : PRIOR FILING DATE: 2002-03-08

: PRIOR APPLICATION NUMBER: US 09/729, 739
 : PRIOR FILING DATE: 2000-12-04

: PRIOR APPLICATION NUMBER: US 09/653, 450
 : PRIOR FILING DATE: 2000-08-31

: PRIOR APPLICATION NUMBER: US 09/620, 312
 : PRIOR FILING DATE: 2000-07-19

: PRIOR APPLICATION NUMBER: US 09/598, 042
 : PRIOR FILING DATE: 2000-06-20

: PRIOR APPLICATION NUMBER: US 09/552, 317
 : PRIOR FILING DATE: 2000-04-25

: PRIOR APPLICATION NUMBER: US 09/488, 725
 : PRIOR FILING DATE: 2000-01-21

: NUMBER OF SEQ ID NOS: 63
 : SOFTWARE: PatentIn version 3.0

: SEQ ID NO 43
 : LENGTH: 927

: TYPE: DNA
 : ORGANISM: Homo sapiens

: US-09-747-835A-43

Alignment Scores:

Pred. No.: 1,07e-106 Length: 927

Score: 1080.00 Matches: 212

Percent Similarity: 81.91% Conservative: 38

Best Local Similarity: 69.41% Mismatches: 53

Query Match: 67.12% Indels: 2

Gaps: 1

US-09-898-586-24 (1-310) x US-09-747-835A-43 (1-927)

QY 1 MetGlyAspAsnIleThrsertIleThrGluPheLeuLeuGlyPheProValGlyPro 20
 DB 1 ATGGTGAAAAATCAGCAATGGTCACAGATTCCTCTACAGGAGATTCTCCGGGCCCA 60
 QY 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPhePheValPheThrLeuGly 40
 DB 61 AGGATTCAGATGCTCCTCTTGGGCTTCTCCCGGTCATATCTTCACCCGTCGGGG 120
 QY 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaPrometTyrPhe 60
 DB 121 AACGGGCGCATCTCGGGGCTCATCTCATGAGATCCAGACCCCATACCCCATGTCCTC 180
 QY 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
 DB 181 TTCCTCTCACCTGCTGCTGTCGACATCGCTACACCCGACAGGAGGTCGCCAGATG 240
 QY 81 LeuValAsnLeuLeuHisProAlaTyrProIleSerPheAlaGlyArgMetMetGlnThr 100
 DB 241 CTGGCAACCTCTGTCATCGACGCAAGCCCATCTCTTGGTGTGATGACGACGAGACC 300

QY 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAsp 120
 DB 301 TTTCCTCTGTTTGGATGTCAGACAGCGAATGCTCTCCGCTGGGAGATGTCAGAT 360
 QY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTyrParValCys 140
 DB 361 CGTTACGTGGCATCTGCCACCCCTCCGATATCCCTCATATGATGACC-----TGTCTAC 414
 QY 141 IleThrLeuAlaValThrSerThrThrThrGlyValLeuLeuSerLeuIleHisLeuVal 160
 DB 415 ATCACTCTGCCATCACTTCTCGACATGTCGTCCTCCCTCGGTATGTCATGTCAGAC 474
 QY 161 LeuLeuLeuProLeuProPheCysArgProGlnTyrIleTyrHisPheCysGluIle 180
 DB 475 CTCATCTTAAGACTGCTCTTGTGGCTGTGAATCAACACCTCTCTCTGTAAGAT 534
 QY 181 LeuAlaValLeuLeuLysLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
 DB 535 CTGCTGTCTCTAGGCTGCTGCTGTCTGATACCTGGCTCAACAGGTGGTCATCTTTCGA 594
 QY 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
 DB 595 GCTGTGATGTCATCTGCTGGGACCACTTGCCTGGTCTGCTCTCATCTGACACATC 654
 QY 221 LeuCysAlaIleLeuGlnIleGlnSerArgGluValGlnArgValAlaPheCysThrCys 240
 DB 655 CTGGCGGCGCATCTGAGATCCAGTCTGGGAGGCGCCAGAAAGGCTTCTTCACACTGC 714
 QY 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260
 DB 715 TCTCTCCACTCTGCTGATGGACTCTTCTTGGCACCGCATCGCATATGATGATGCC 774
 QY 261 ProArgTyrGlyAsnProLysGlnIleLysTyrIleLeuLeuPheHisSerLeuPhe 280
 DB 775 CTAAGTCCCGCCATCTCTGAGACGACGAGAAGGTCCTTTTATTTTACATGCTTTC 834
 QY 281 AsnProMetLeuAsnProLeuIleCysSerLeuArgAsnSerGlyValLysAsnThrLeu 300
 DB 835 AACCGGCTCAACCCCTGATTACACTGAGAGATGTAGAGTCAAGGATGCCCTG 894
 QY 301 LysArgValIleu 304
 DB 895 AGGAGGACACTG 906

RESULT 12
 US-09-747-835A-41
 : Sequence 41, Application US/09747835A
 : Patent No. US2002014692A1
 : GENERAL INFORMATION:
 : APPLICANT: Yamazaki, Victoria
 : APPLICANT: Tang, Y. Tom
 : APPLICANT: Liu, Chenghua
 : APPLICANT: Zhou, Ping
 : APPLICANT: Wang, Dunrui
 : APPLICANT: Zhang, Jie
 : APPLICANT: Ren, Feiyun
 : APPLICANT: Asundi, Vinod
 : APPLICANT: Drmanac, Radoje T
 : TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-L
 : FILE REFERENCE: HYS-37CIP
 : POLYPEPTIDES AND POLYNUCLEOTIDES
 : CURRENT APPLICATION NUMBER: US/09/747, 835A
 : PRIOR FILING DATE: 2002-03-08
 : PRIOR APPLICATION NUMBER: US 09/729, 739
 : PRIOR FILING DATE: 2000-12-04
 : PRIOR APPLICATION NUMBER: US 09/653, 450
 : PRIOR FILING DATE: 2000-08-31
 : PRIOR APPLICATION NUMBER: US 09/620, 312
 : PRIOR FILING DATE: 2000-07-19
 : PRIOR APPLICATION NUMBER: US 09/598, 042
 : PRIOR FILING DATE: 2000-06-20
 : PRIOR APPLICATION NUMBER: US 09/552, 317

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; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 1782
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (485)..(1411)
US-09-747-835A-41

```

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Alignment Scores:
Pred. No.: 2,74e-106 Length: 1782
Score: 1080.00 Matches: 211
Percent Similarity: 81.91% Conservative: 38
t Local Similarity: 69.41% Mismatches: 53
Query Match: 67.12% Indels: 2
Gaps: 1

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US-09-898-586-24 (1-310) x US-09-747-835A-41 (1-1782)

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QY 1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuLeuGlyPheProValGlyPro 20
DB 485 ATGGTCAAAATCAGACATGTCACAGAGTTCCTCTACTGGGATTTCTCTGGGCCCA 544
QY 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuLeuGly 40
DB 545 AGGATTCACATGCTCTCTGGGCTCTCTCCCTGTTATATCTTACCCCTGGGG 604
QY 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuIleIslaProMetTyrPhe 60
DB 605 AACGGGGCATCTCTGGGCTCATCTCACTGACATCCAGACTCATGCCCATGTACTTC 664
QY 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
DB 665 TTCTCTGACCTGCTGCTGTCACATCGCTACACCCGACGGATGCGCCAGATG 724
QY 81 LeuValAspLeuLeuHisProAlaIleProIleSerPheAlaGlyArgMetGlnThr 100
DB 725 CTGGGACATCTCTGATCCAGCCAGCCCATCTCTCTGCTGTTGATGACGGAC 784
QY 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValValMetSerTyrAsp 120
DB 785 TTTCCTGTTTGAAGTTTGGACACAGCAATGTCCTGCTGGTGGTGTGATGCTACGAT 844
QY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTyrArgValCys 140
DB 845 CGTTAGTCGACATCTGCCACCCCTCGATACATCCGTCATCATGACC-----TGCTGC 898
QY 141 IleThrLeuAlaValThrSerThrThrThrGlyValLeuLeuSerLeuIleHisVal 160
DB 899 ATGACTCTGGCATCATCTCCGACATGTCGCTCCCTGCTGATGTCATGTCAGAC 958
QY 161 LeuLeuLeuProLeuProPheCysArgProGlnIleTyrHisPhePheCysGluIle 180
DB 959 CTCATCTTAAGATGCCCTTTTGGCTGTCGTAATCAACCATCTTCTTGGAATC 1018
QY 181 LeuAlaValLeuLeuAlaCysAlaAspThrHisIleAsnGluAsnMetValLeuAla 200
DB 1019 CTGTGTCCTCCTGAGCTGCTGCTGATACCTGCTGATCAACCAAGGTCATCTTGTGA 1078
QY 201 GlyAlaIleSerGlyLeuValGlyProLeuSerThrIleValValSerTyrMetCysIle 220
DB 1079 GCGTCGATGTTATCTGATGGACACTCTGCTGGTGGTGGTCTCTACATCACACATC 1138
QY 221 LeuCysAlaIleLeuGlnIleGlnSerArgIleValGlnArgIleAlaPheCysThrCys 240
DB 1139 CTGGGCGCATCTCTGAGGTCCAGTCTGGGACGGCCGCAAGAGCTTCTTCCACTTCC 1198
QY 241 PheSerHisLeuCysValIleGlyLeuPheTyrGlyThrAlaIleIleMetTyrValGly 260

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DB 1199 TCCCTCCACCTCTGCTAGTGGGACTCTTCTTGGCAGGGCAATCGTCATCATGCGCC 1258
QY 261 ProArgTyrGlyAsnProIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 280
DB 1259 CCTAAGTCCGGCCATCTCTGAGAGCAGCAAGAGTCTTCTTCTTCTTCTTCTTCTTCT 1318
QY 281 AsnProMetLeuAsnProLeuIleCysSerLeuAlaArgAsnSerGluValAlaAsnThrLeu 300
DB 1319 AACCGATGCTAAACCCCTGATTTACAACTGAGGAATGTAGAGTCAAGGTGCGCTTG 1378
QY 301 LysArgValLeu 304
DB 1379 AGGAGAGCAGCTG 1390

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RESULT 13

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US-09-886-055-484
; Sequence 484, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STYER, LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886, 055
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213, 812
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 484
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-886-055-484

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Alignment Scores:
Pred. No.: 3.66e-97 Length: 933
Score: 991.00 Matches: 189
Percent Similarity: 77.42% Conservative: 51
Best Local Similarity: 60.97% Mismatches: 70
Query Match: 61.59% Indels: 0
Gaps: 0

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US-09-898-586-24 (1-310) x US-09-886-055-484 (1-933)

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QY 1 MetGlyAspAsnIleThrSerIleThrGluPheLeuLeuLeuGlyPheProValGlyPro 20
DB 1 ATGGAAACAAATCAGACCTGATCAGAGATCTCTTGGGATTCACAGTGGACCCA 60
QY 21 ArgIleGlnMetLeuLeuPheGlyLeuPheSerLeuPheTyrValPheThrLeuLeuGly 40
DB 61 GCTCGAGATTCCTCTCTTGGGCTTCTTCTGATTTCTGATTTCTGATTTCTGATTTCTGAT 120
QY 41 AsnGlyThrIleLeuGlyLeuIleSerLeuAspSerArgLeuHisAlaProMetTyrPhe 60
DB 121 AATGGATTAATCTCGGGCTATCTACTGCTTACAGTCAACACCATATGATGTC 180
QY 61 PheLeuSerHisLeuAlaValAlaAspIleAlaTyrAlaCysAsnThrValProArgMet 80
DB 181 TTCTGTCACACTGGCCATGTCGATGTCATGCTGATGTCGATGTCGATGTCGATGTCGAT 240
QY 81 LeuValAsnLeuLeuHisProAlaIleProIleSerPheAlaGlyArgMetGlnThr 100
DB 241 CTAGCAAAATCTTGTGATGACCAAAAAGTATCTCTTGTGCTCTTGCATATCTACAGCT 300
QY 101 PheLeuPheSerThrPheAlaValThrGluCysLeuLeuValAlaMetSerTyrAsp 120
DB 301 TTTTGTGATTTGGCTTTGCTATACAGACTGCTGATTTGGTATGATGATGCTGATGAT 360
QY 121 LeuTyrValAlaIleCysHisProLeuArgTyrLeuAlaIleMetThrTyrArgValCys 140

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